Page 9, line 30, change "occurrances" to -- occurrences --.

Page 13, line 21, change "positons" to -- positions --.

IN THE ABSTRACT

Please insert the attached Abstract consisting of a single sheet with the application papers.

IN THE CLAIMS

Cancel without prejudice claim 1 and add thereto the following new claims:

-- 17. An apparatus for analysing a polynucleotide, the apparatus comprising an impermeable support segregated into at least two defined cells, the cells having oligonucleotides covalently attached thereto, wherein the sequence of the oligonucleotides of a first cell is different from the sequence of the oligonucleotides of a second cell.

18. The apparatus of claim 17, wherein the length of each oligonucleotide is from 8 to 20 nucleotides.

19. The apparatus of claim 17, wherein the cells have a size of about 10μm to about 100μm.

20. The apparatus of claim 17, wherein the cells are separated by a solvent-repellent grid.

21. The apparatus of claim 17, wherein the impermeable support is glass.

22. The apparatus of claim 17, wherein each oligonucleotide is bound to the support by a covalent link through a terminal nucleotide.

23. The apparatus of claim 17, comprising between 72 and 10^{12} cells.

24. The apparatus of claim 17, comprising 4^s oligonucleotide sequences of length *s*, wherein $s \geq 4$, and comprises 4^s cells.

25. The apparatus of claim 17, wherein the oligonucleotides in the cells have overlapping sequences for mismatch scanning of the polynucleotide.

26. An apparatus for analysing a polynucleotide, the apparatus comprising an impermeable glass plate with patches of microporous glass, the patches defining cells of an array, each cell having oligonucleotides covalently attached thereto, wherein the sequence of the oligonucleotides of a first cell is different from the sequence of the oligonucleotides of a second cell.

27. The apparatus of claim 26, wherein the length of each oligonucleotide is from 8 to 20 nucleotides.

28. The apparatus of claim 26, wherein the cells have a size of about 10μm to about 100μm.

29. The apparatus of claim 26, wherein each oligonucleotide is bound to a patch by a covalent link through a terminal nucleotide.

SUB C2 30. The apparatus of claim 26, comprising between 72 and 10^{12} cells.

31. The apparatus of claim 26, comprising 4^s oligonucleotide sequences of length *s*, wherein $s \geq 4$, and comprises 4^s cells.

32. The apparatus of claim 26, wherein the oligonucleotides in the cells have overlapping sequences for mismatch scanning of the polynucleotide.

33. A method for analysing a polynucleotide, comprising the steps of:

labelling the polynucleotide or fragments of the polynucleotide, to produce labelled nucleic acid;

applying the labelled nucleic acid under hybridisation conditions to the array of claim 17, and

observing the cells in the array to which the labelled nucleic acid hybridises.

34. The method of claim 33, wherein the polynucleotide is randomly degraded to form a mixture of oligonucleotides of chosen lengths, the mixture being thereafter labelled to form labelled nucleic acid which is applied to the array.

35. The method of claim 33, wherein the polynucleotide or fragments of the polynucleotide are labelled with ^{32}P or a fluorescent label.

36. The method of claim 33, wherein the polynucleotide or fragments of the polynucleotide are populations of mRNA, genomic DNA, or PCR products.

37. A method for analysing a polynucleotide, comprising the steps of:

labelling the polynucleotide or fragments of the polynucleotide, to produce labelled nucleic acid;

applying the labelled nucleic acid under hybridisation conditions to the array of claim 26; and

observing the cells in the array to which the labelled nucleic acid hybridises.

38. The method of claim 37, wherein the polynucleotide is randomly degraded to form a mixture of oligonucleotides of chosen lengths, the mixture being thereafter labelled to form labelled nucleic acid which is applied to the array.